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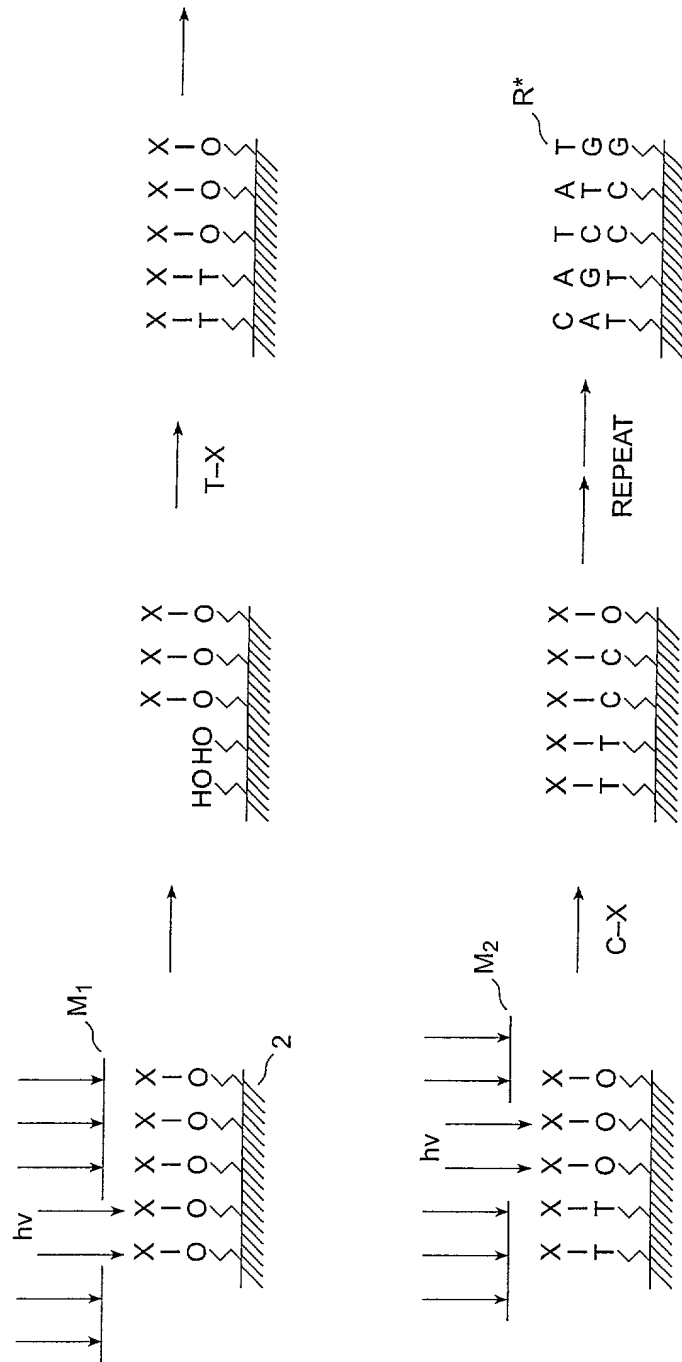


FIG. 1

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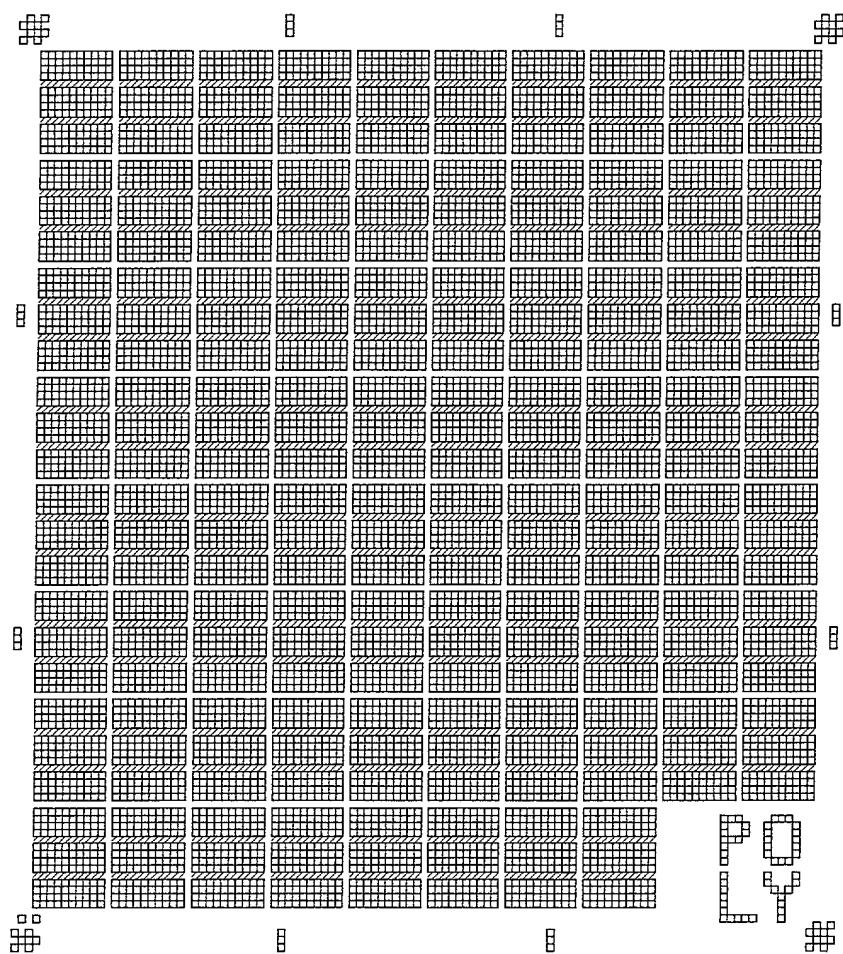
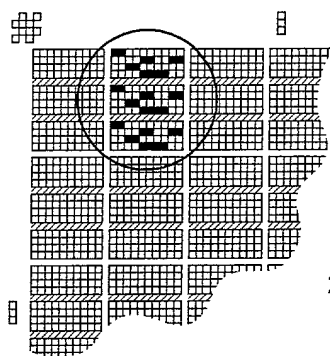


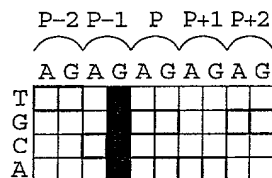
FIG. 2A



SEQUENCE AT POLYMORPHISM WI-567

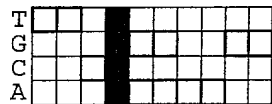
5' TGCTGCCTTGGTTC [A/G] AGCCCTCATCTCTTT 3'

THREE BLOCKS OF COMPLEMENTARY
20-MER OLIGOS WITH SUBSTITUTIONS (N)
7, 10 AND 13 BP FROM THE 3' END



BASES IN THE SHADED COLUMNS

3' BLOCK 20/7 5'
AACCAAN[C] TCGGGAGTAGAG



3' BLOCK 20/10 5'
CGGAACCAAN[C] TCGGGAGTA



3' BLOCK 20/13 5'
CGACGGAACCAAN[C] TCGGGA

FIG. 2B

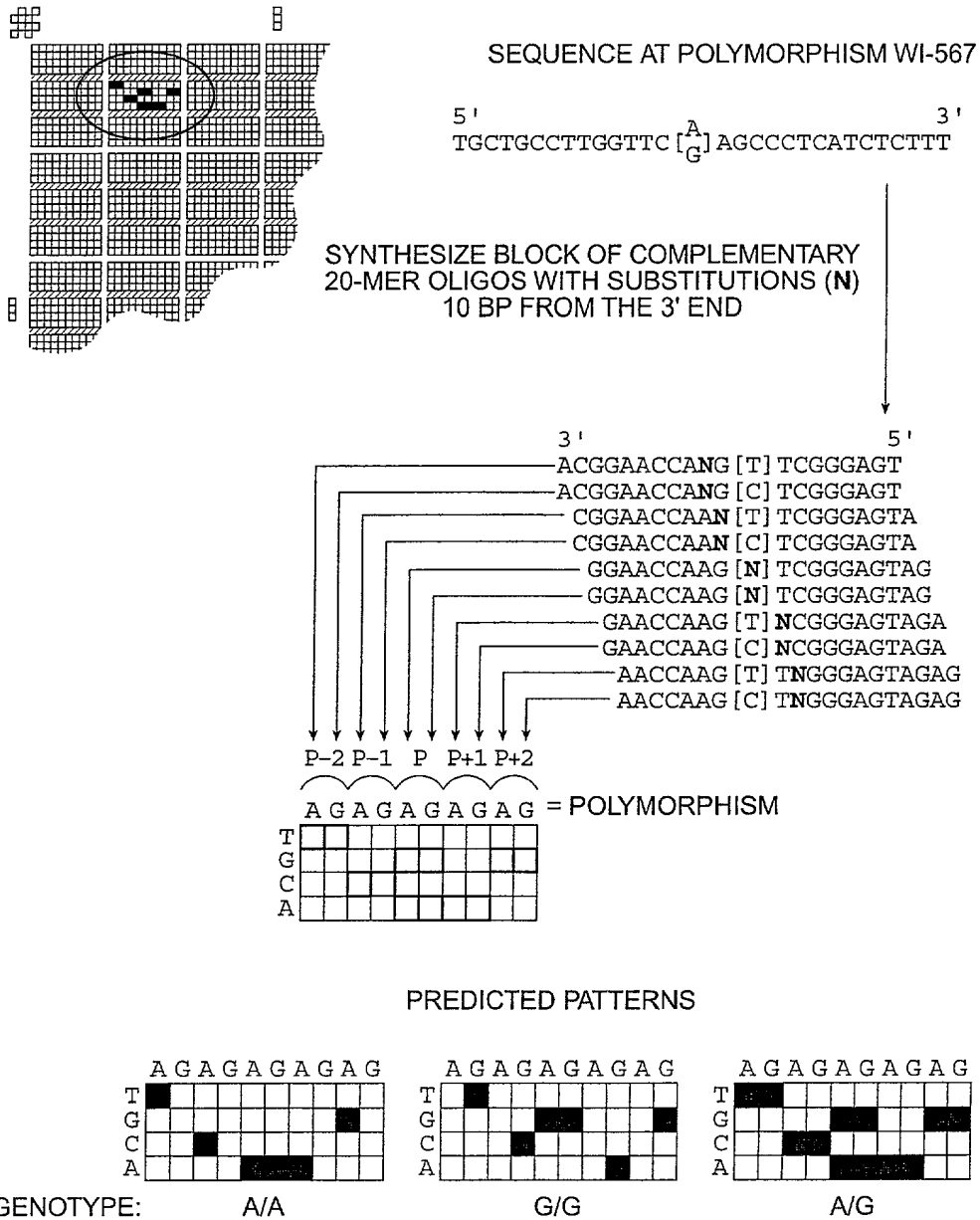


FIG. 3

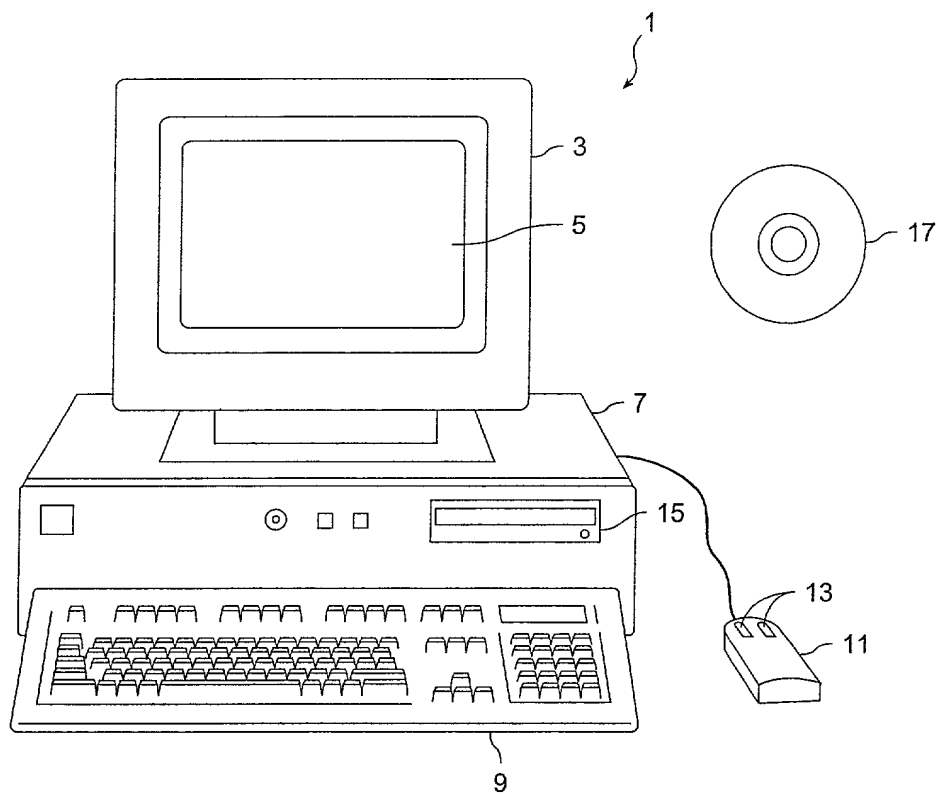


FIG. 5

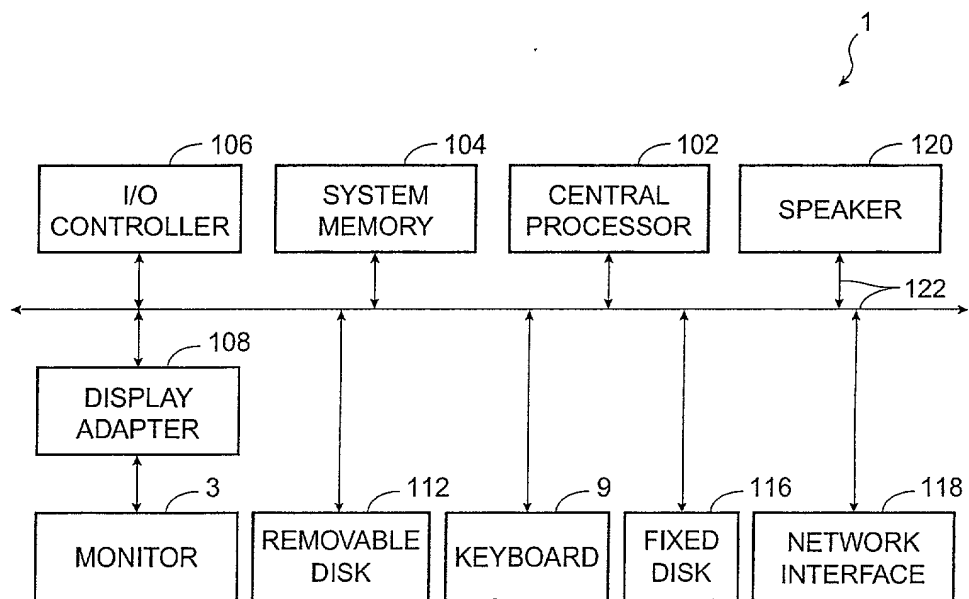


FIG. 6

	P-2		P-1	P0	P+1	P+2
	X Y		X Y	X Y	X Y	X Y
A						
C						
G						
T						

FIG. 7

	T		C		A		G
	A	G	A	G	A	G	A
A	nd	nd	nd	nd	nd	nd	nd
C	nd	nd	DD	nd	nd	nd	nd
G	nd	nd	nd	nd	nd	nd	nd
T	nd	nd	NN	nd	nd	nd	nd

FIG. 8

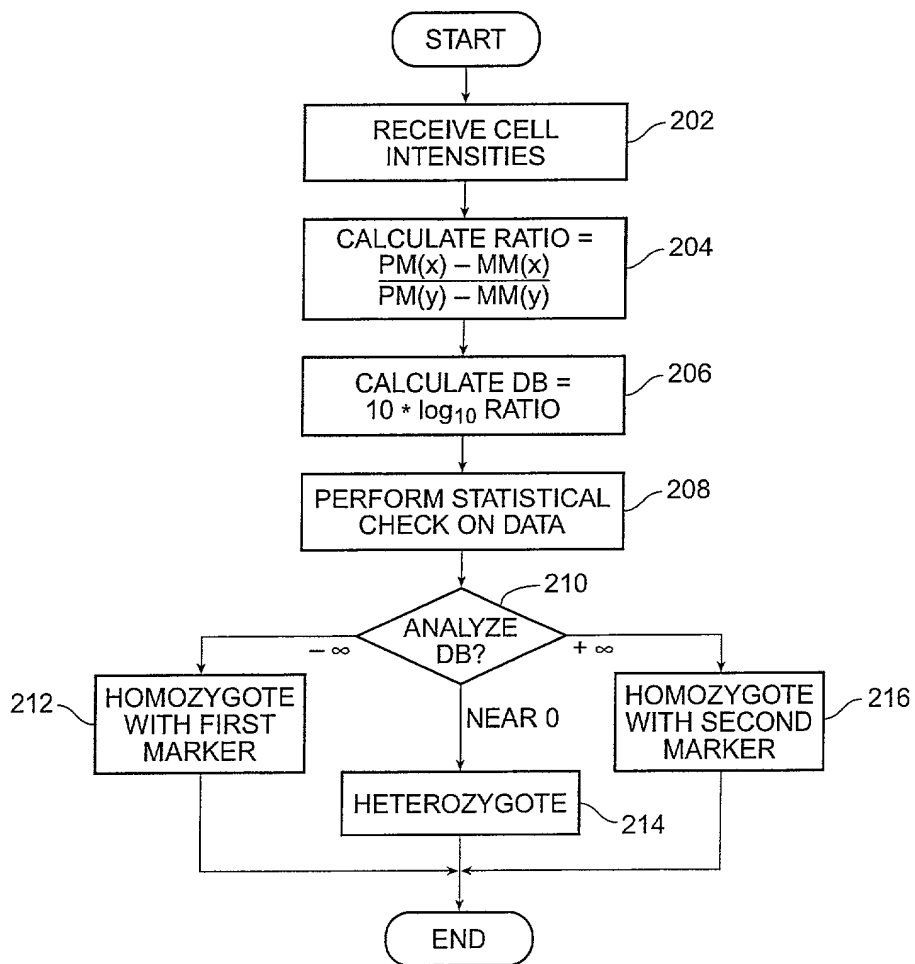


FIG. 9

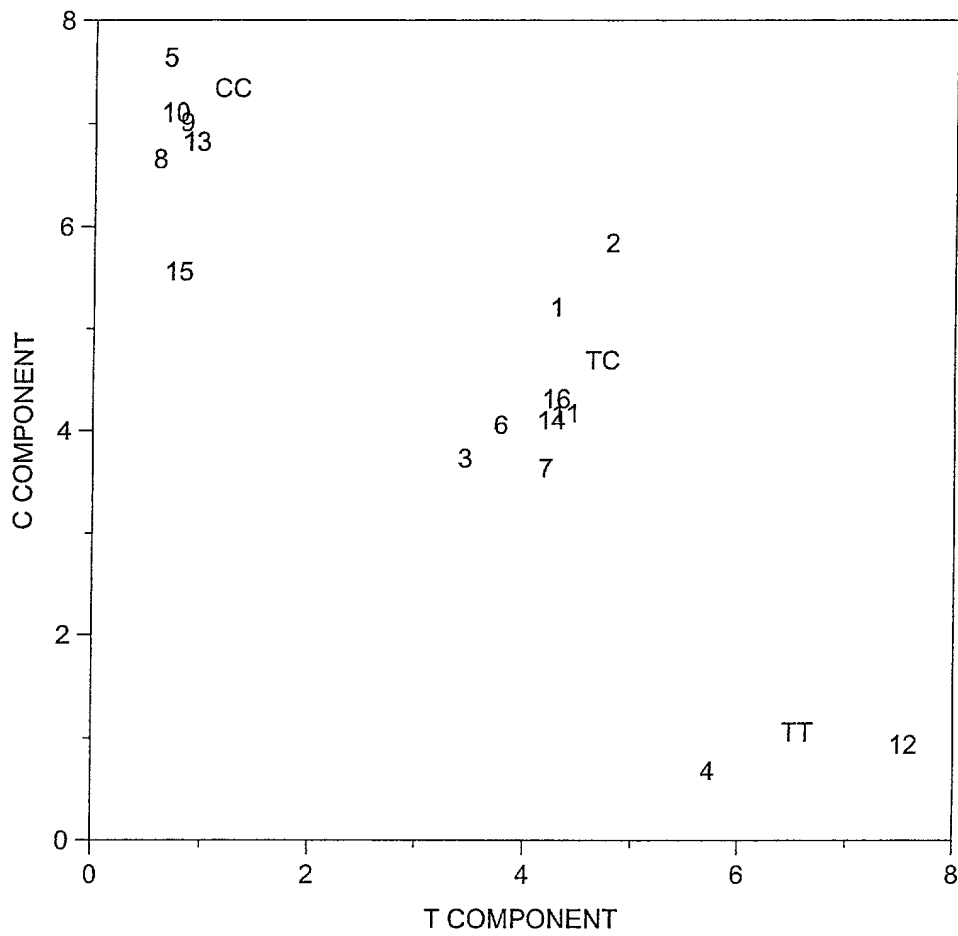
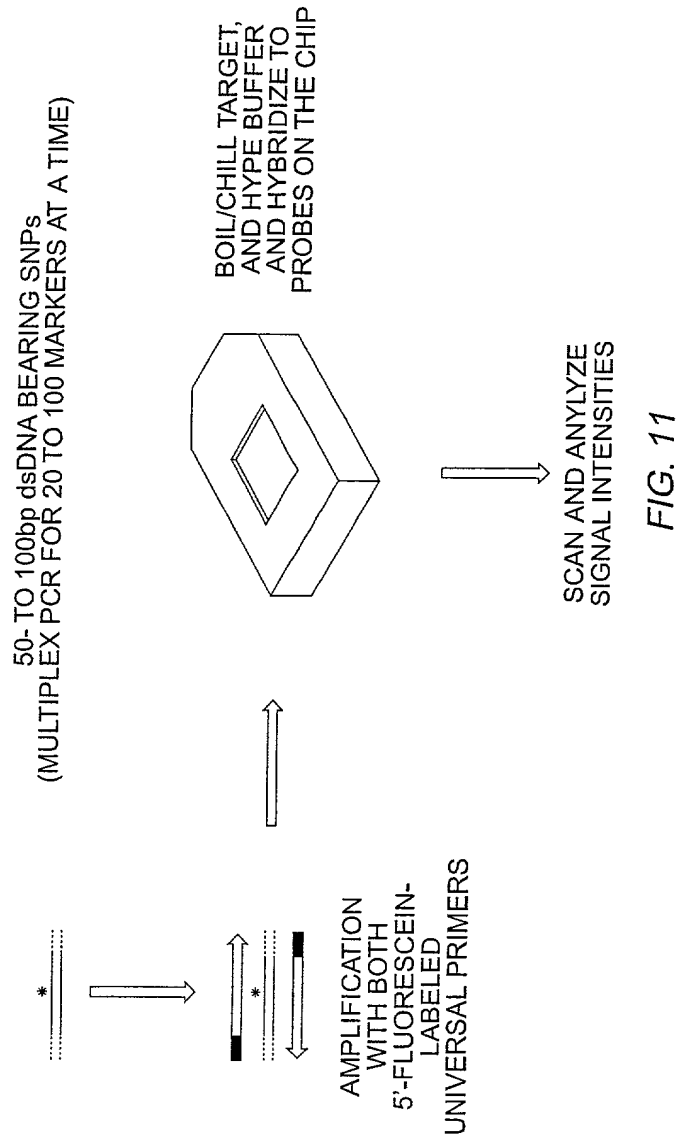


FIG. 10

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10/10

$$\begin{aligned}
 \text{DB} &= \text{"DECIBELS"} &= 10 \times \text{LOG (DETECTION RATIO)} \\
 \text{DETECTION RATIO} &= \frac{\text{A PERFECT MATCH} - \text{A MISMATCHES}}{\text{B PERFECT MATCH} - \text{B MISMATCHES}} \\
 \text{C} = \text{SIGNIFICANCE CHECK} &= \frac{\text{MAX (A OR B PERFECT MATCH)}}{\sigma (\text{A OR B MISMATCHES})} > 2 \\
 \text{P} = \text{PATTERN MATCHING} &= \frac{\text{MEAN [MAX (A OR B PERFECT MATCHES)]}}{\text{MEAN [MAX(A OR B MISMATCHES)]}} > 1.2
 \end{aligned}$$

PREDICTED PATTERNS

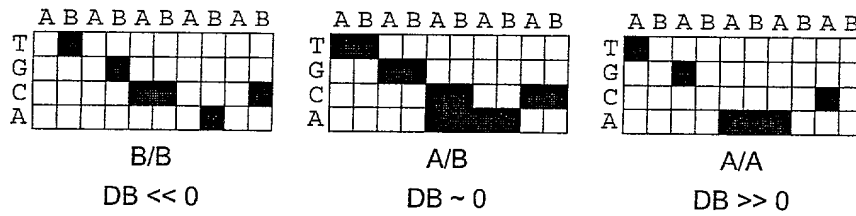


FIG. 12

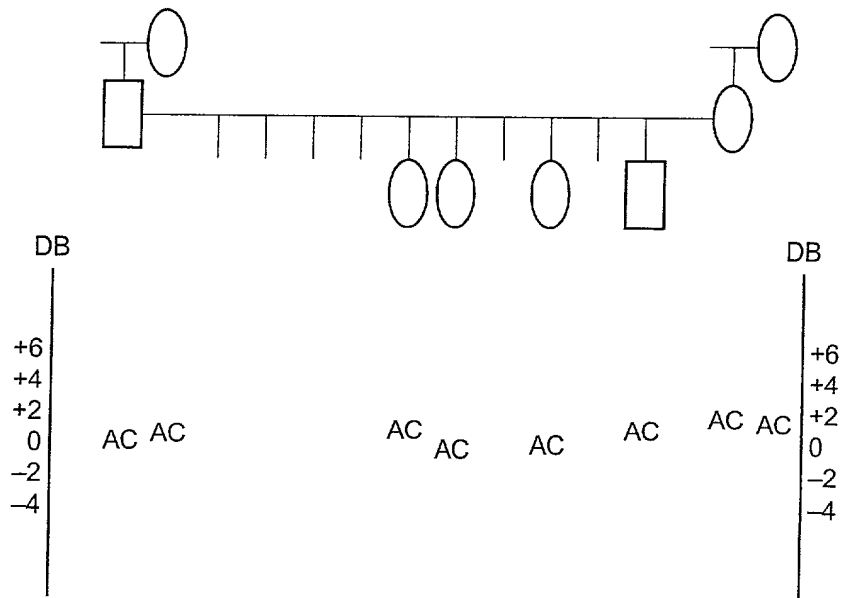


FIG. 13